

## WEST Search History

DATE: Tuesday, June 22, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L8	L6 same (substitution\$)	15
<input type="checkbox"/>	L7	L6 same (i adj domain)	24
<input type="checkbox"/>	L6	L5 same integrin	714
<input type="checkbox"/>	L5	baised or open or closed or conformation	4222229
<input type="checkbox"/>	L4	SPRINGER-TIMOTHY.in.	7
<input type="checkbox"/>	L3	SHIMAOKA-MOTOMU.in.	2
<input type="checkbox"/>	L2	SHIFMAN-JULIA.in.	1
<input type="checkbox"/>	L1	MAYO-STEPHEN.in.	8

END OF SEARCH HISTORY

=> d his

(FILE 'HOME' ENTERED AT 13:01:33 ON 22 JUN 2004)

FILE 'DISSABS, IMOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,  
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,  
MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,  
ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 13:01:50 ON  
22 JUN 2004

L1           E MAYO STEPHEN?/AU  
          3 S E1 OR E2  
L2           E SHIFMAN JULIA?/AU  
          16 S E1 OR E2  
          E SHIMAOKA MOTOMU?/AU  
L3       153737 S E 2  
L4           96 S E2  
          E SPRINGER TIMOTHY?/AU  
L5       4367 S (OPEN OR CLOSED OR CONFORMATION) (S) INTEGRIN?  
L6       308 S L5 (S) (I (A) DOMAIN)  
L7       104 DUP REM L6 (204 DUPLICATES REMOVED)  
L8       19 S L7 AND (139 OR 153 OR 157 OR 160 OR 215)

=>

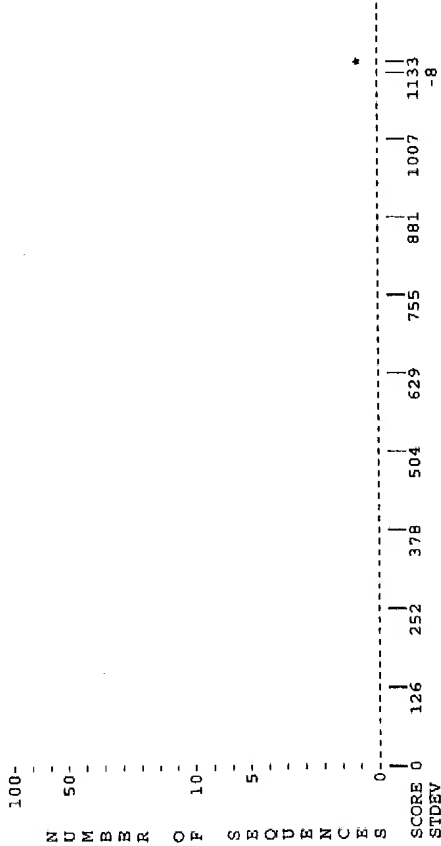
> O < IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-902-481b-1.res made by jdelaval on Tue 22 Jun 104 7:02:54-PDT.

Query sequence being compared: US-09-902-481B-1 (1-1153)  
Number of sequences searched: 4  
Number of scores above cutoff: 4

Results of the initial comparison of US-09-902-481B-1 (1-1153) with:  
File : seq3-seq4-seq5-seq6.pap



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1128	1129	3.70
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00
Number of residues:		4548	
Number of sequences searched:		4	
Number of scores above cutoff:		4	

The scores below are sorted by initial score.  
Significance is calculated based on initial score.  
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame
1. US-09-902-481B-6	Sequence 6, Application U 1137 1133	1133	1.35	0	
2. US-09-902-481B-5	Sequence 5, Application U 1137 1129	1129	0.27	0	
3. US-09-902-481B-4	Sequence 4, Application U 1137 1128	1128	0.00	0	
4. US-09-902-481B-3	Sequence 3, Application U 1137 1124	1124	-1.08	0	

1. US-09-902-481B-1 (1-1153)  
US-09-902-481B-6 Sequence 6, Application US/09902481B  
Sequence 6, Application US/09902481B  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy  
APPLICANT: Shimaoka, Motomu  
APPLICANT: Shifman, Julia  
APPLICANT: Kayo, Stephen  
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY  
FILE REFERENCE: A-70586-1/RPT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/902,481B  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/216,600  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 1137  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic

Initial Score = 1133 Optimized Score = 1133 Significance = 1.35  
Residue Identity = 99% Matches = 1133 Mismatches = 4  
Gaps = 0 Conservative Substitutions = 0

10 X 20 30 40 50 60 70  
MALRVLLTALTCHEGPNLDTENAMTFQENARGFGQSVVLOGSRVVGAPQEIIVAAORGSLYQCDYSTGS  
X 10 20 30 40 50 60 70  
FNLDTENAMTFQENARGFGQSVVLOGSRVVGAPQEIIVAAORGSLYQCDYSTGS  
X 10 20 30 40 50 60 70  
80 90 100 110 120 130 140  
CEPIRLQVPEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTVVKGLCPFLGSLNLRQQPKPFPEALRGCC  
|||||  
60 70 80 90 100 110 120  
CEPIRLQVPEAVNMSLGLSLAATTSPPOLLACGPTVHQTCSNTVVKGLCPFLGSLNLRQQPKPFPEALRGCC  
150 160 170 180 190 200 210  
PQSDIAFLIDGSGSIIIPHDPRMKEFVSTVMEQLKSKTKLFSLMQYSEEFRIHFTPFKEFQNNPNRSLVK  
|||||  
130 140 150 160 170 180 190 200  
PQSDIAFLIDGSGSIIIPHDPRMKEFVSTVMEQLKSKTKLFSLMQYSEEFRIHFTPFKEFQNNPNRSLVK  
220 230 240 250 260 270 280  
PITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVG  
|||||  
210 220 230 240 250 260 270  
PITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGVEDVPEADREGVIRYVIGVG  
290 300 310 320 330 340 350 360  
DAFRSEKSRQELNTIASKPPRDHVFQVNNPFAKLTIONQLREKIIFAIEGTQTSSSPFHEMSQEGFSAAIT  
|||||  
280 290 300 310 320 330 340  
DAFRSEKSRQELNTIASKPPRDHVFQVNNPFAKLTIONQLREKIIFAIEGTQTSSSPFHEMSQEGFSAAIT  
370 380 390 400 410 420 430  
SNGPLLSTVGSYDWAGGVFLYTSKESKSTPINTVRVSDMDAYLGLTAAAILLRNVOSLVGLGAPRICHIGLV  
|||||

Sequence 5, Application US/09902481B  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy  
APPLICANT: Shimada, Motomu  
APPLICANT: Shimada, Motomu  
APPLICANT: Shimada, Motomu  
APPLICANT: Shimada, Motomu  
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY  
FILE REFERENCE: A-70586-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/902,481B  
PRIOR APPLICATION NUMBER: 2001-07-09  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 1137  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
Initial Score = 1129 Optimized Score = 1129 Significance = 0.27  
Residue Identity = 93% Matches = 1129 Mismatches = 8  
Gaps = 0 Conservative Substitutions = 0  
MALRVLTLTALTLCHGFENLQENAMTQENARGFQSVVQLQGSRRVVGAPQEIIVAAANQSGSLYQCDYSTGS  
10 X 20 30 40 50 60 70  
FNLQENAMTQENARGFQSVVQLQGSRRVVGAPQEIIVAAANQSGSLYQCDYSTGS  
X 10 20 30 40 50  
CEPIRLQVPVEAVNMSLGLSLAATSPQALLACGPTVHTCSENTYKGLCFGLGSLNLRQOPQFPPEALRGC  
80 90 100 110 120 130 140  
CEPIRLQVPVEAVNMSLGLSLAATSPQALLACGPTVHTCSENTYKGLCFGLGSLNLRQOPQFPPEALRGC  
60 70 80 90 100 110 120  
POEDSDIAFLDGGSGSIIPHDPRRAKEPISTWMLQAKSKTLFSLMOYSEEFRIHTFKPQNNPNRSLIK  
150 160 170 180 190 200 210  
POEDSDIAFLDGGSGSIIPHDPRRAKEPISTWMLQAKSKTLFSLMOYSEEFRIHTFKPQNNPNRSLIK  
130 140 150 160 170 180 190 200  
PITQLLGTHTATGIRKVVRELFNITNGARKNAFKILITLTDGKFGDPLGYEDVIPADREGVIRYVIGVG  
220 230 240 250 260 270 280  
PITQLLGTHTATGIRKVVRELFNITNGARKNAFKILITLTDGKFGDPLGYEDVIPADREGVIRYVIGVG  
210 220 230 240 250 260 270  
DAFSEKSRQELNTIASPPRDHVPQNNPEALKTIONLREKIPAEGTOTGSSSSPEHEMSQBFSAAIT  
290 300 310 320 330 340 350  
DAFSEKSRQELNTIASPPRDHVPQNNPEALKTIONLREKIPAEGTOTGSSSSPEHEMSQBFSAAIT  
280 290 300 310 320 330 340  
SNGLPLSTVGSVDWAGGVFLYTSKEKSTFINMTVDSDMDNDAYLGYAAAILLRNVQSLVGLGAPYQHIGLV  
370 380 390 400 410 420 430  
SNGLPLSTVGSVDWAGGVFLYTSKEKSTFINMTVDSDMDNDAYLGYAAAILLRNVQSLVGLGAPYQHIGLV  
350 360 370 380 390 400 410  
AMFRONTGWESNANVKGTQICAVFGASLCSVDVDSNGSTDLVLIAGAPHYETQTRGGVSVCPPLRGRARW  
440 450 460 470 480 490 500  
AMFRONTGWESNANVKGTQICAVFGASLCSVDVDSNGSTDLVLIAGAPHYETQTRGGVSVCPPLRGRARW  
420 430 440 450 460 470 480  
QCDVLYGEGQGPWCFRGAALTVDVNGDKLTDAICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK  
510 520 530 540 550 560 570  
QCDVLYGEGQGPWCFRGAALTVDVNGDKLTDAICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK  
490 500 510 520 530 540 550 560

580 590 600 610 620 630 640  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
570 580 590 600 610 620 630  
650 660 670 680 690 700 710 720  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
640 650 660 670 680 690 700 710  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC  
710 720 730 740 750 760 770 780 790  
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS  
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS  
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS  
780 790 800 810 820 830 840 850 860  
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRTNKTQFQLELPVKYAVVMTSHGVS  
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRTNKTQFQLELPVKYAVVMTSHGVS  
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMPRTNKTQFQLELPVKYAVVMTSHGVS  
870 880 890 900 910 920 930 940 950 960 970 980 990  
TKYLNPTASENTSRMWHQYQVSNLQSRSLPISLFLVPLVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH  
TKYLNPTASENTSRMWHQYQVSNLQSRSLPISLFLVPLVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH  
TKYLNPTASENTSRMWHQYQVSNLQSRSLPISLFLVPLVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH  
940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060  
SDFLAELKAPVNCSTAVCORIQDIPFCQIOEFNATKGNLSPDWYIKTSHNLLIVSTABILFNDVSF  
SDFLAELKAPVNCSTAVCORIQDIPFCQIOEFNATKGNLSPDWYIKTSHNLLIVSTABILFNDVSF  
SDFLAELKAPVNCSTAVCORIQDIPFCQIOEFNATKGNLSPDWYIKTSHNLLIVSTABILFNDVSF  
1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150  
TLPCQGAFFVSQETKVEPEVPEVPLPLVGVSSVGGLLLLALITAAALYKLGFFKROVKMMSEGGPPGARP  
TLPCQGAFFVSQETKVEPEVPEVPLPLVGVSSVGGLLLLALITAAALYKLGFFKROVKMMSEGGPPGARP  
TLPCQGAFFVSQETKVEPEVPEVPLPLVGVSSVGGLLLLALITAAALYKLGFFKROVKMMSEGGPPGARP  
1070 1080 1090 1100 1110 1120 1130 1140 1150  
X  
Q  
Q  
Q  
X

3. US-09-902-481B-1 (1-1153)  
US-09-902-481B-4 Sequence 4, Application US/09902481B

Sequence 4, Application US/09902481B

GENERAL INFORMATION:  
APPLICANT: Springer, Timothy  
APPLICANT: Shimooka, Motomu  
APPLICANT: Shifman, Julia  
APPLICANT: Mayo, Stephen  
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY  
FILE REFERENCE: A-70586-1/RPT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/502,481B  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/216,600  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4

LENGTH: 1137  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
Initial Score = 1128 Optimized Score = 1128 Significance = 0.00  
Residue Identity = 99% Matches  
Gaps = 0 Conservative Substitutions  
10 X 20 30 40 50 60 70  
MALRVLLLTALATICHGFLNDTENAMTFQENARGFGQSVVQLOGSRVVGAPQBIVAANORGSLYQCDYSTGS  
PNILOTENAMTFQENARGFGQSVVQLOGSRVVGAPQBIVAANORGSLYQCDYSTGS  
X 10 20 30 40 50  
80 90 100 110 120 130 140  
CEPIRLQVPEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQQPKPFPEALRGC  
CEPIRLQVPEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQQPKPFPEALRGC  
60 70 80 90 100 110 120 130 140  
CEPIRLQVPEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQQPKPFPEALRGC  
150 160 170 180 190 200 210  
POQSDIAFLIDGSGSIIIPHDPRMKEFVSTYMEQLKSKTLFSLMOYSEEPRIHFTFKFQNNPNSRLVK  
POQSDIAFLIDGSGSIIIPHDPRMKEFVSTYMEQLKSKTLFSLMOYSEEPRIHFTFKFQNNPNSRLVK  
130 140 150 160 170 180 190 200  
POQSDIAFLIDGSGSIIIPHDPRMKEFVSTYMEQLKSKTLFSLMOYSEEPRIHFTFKFQNNPNSRLVK  
220 230 240 250 260 270 280  
PITQLLGRTHATGIRKRVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVITPEADREGVIRYVIGV  
PITQLLGRTHATGIRKRVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVITPEADREGVIRYVIGV  
210 220 230 240 250 260 270  
PITQLLGRTHATGIRKRVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVITPEADREGVIRYVIGV  
290 300 310 320 330 340 350 360  
DAFRSEKSRDELNTIASKPRDHVQVNNFEALKTTONQLREKIFAIEGTQTGSSSSFEHMSQEGESAALT  
DAFRSEKSRDELNTIASKPRDHVQVNNFEALKTTONQLREKIFAIEGTQTGSSSSFEHMSQEGESAALT  
280 290 300 310 320 330 340  
DAFRSEKSRDELNTIASKPRDHVQVNNFEALKTTONQLREKIFAIEGTQTGSSSSFEHMSQEGESAALT  
370 380 390 400 410 420 430  
SNQPLLSVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILLRNVQSLVGLAPRYOHIGLV  
SNQPLLSVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILLRNVQSLVGLAPRYOHIGLV  
350 360 370 380 390 400 410  
SNQPLLSVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILLRNVQSLVGLAPRYOHIGLV  
440 450 460 470 480 490 500  
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW  
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW  
420 430 440 450 460 470 480  
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW  
510 520 530 540 550 560 570  
QCDVAVYXGEOGPKGFRGMAALTVDLGVNGDKLTVAIGAPQEDNRCGAVYLFHGTSGSGISPSHSQRIAGSK  
QCDVAVYXGEOGPKGFRGMAALTVDLGVNGDKLTVAIGAPQEDNRCGAVYLFHGTSGSGISPSHSQRIAGSK  
490 500 510 520 530 540 550 560  
QCDVAVYXGEOGPKGFRGMAALTVDLGVNGDKLTVAIGAPQEDNRCGAVYLFHGTSGSGISPSHSQRIAGSK  
580 590 600 610 620 630 640  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
570 580 590 600 610 620 630  
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQGHVLLRSQPLVRVKAIMEFNEPREVARNVPECDQVWKGKE  
650 660 670 680 690 700 710 720  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKNSRTRQTVGLGTQTCETLKLQLP  
730 740 750 760 770 780 790  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC  
NCIEDPVPSPVLRNLFNSLVTGTPSAFNGLPVLAEDAQRFTALFPPEKCKGNDNICODDLSTFSPMSLDC

NCIEDPVSPIVRLNFSVLGTPLSAGNRLVLAEDAQRLLTALPPEKCKGNDNICQDDLSITFSPMSLDC  
710 720 730 740 750 760 770  
LVVGGPRFNVTVVRNDGDSYRTQVTFPPFLDLSYRKVSTLQNSQSRWRLACESASSTEVSGALKSTS  
800 810 820 830 840 850 860  
LVVGGPRFNVTVVRNDGDSYRTQVTFPPFLDLSYRKVSTLQNSQSRWRLACESASSTEVSGALKSTS  
780 790 800 810 820 830 840  
CSINHIPPENSEVTNITFDVDSKASIGNKLLKANVTSENNPRNTKTFQLELPVKYAVYVWVTHSGVS  
870 880 890 900 910 920 930  
CSINHIPPENSEVTNITFDVDSKASIGNKLLKANVTSENNPRNTKTFQLELPVKYAVYVWVTHSGVS  
850 860 870 880 890 900 910 920  
TKYLNFTASENTRSMOQYQVSNLQSRSLPISLVLVPLVRLNQTVIWRDQVTFSENLSTCHTKERLPSH  
940 950 960 970 980 990 1000  
TKYLNFTASENTRSMOQYQVSNLQSRSLPISLVLVPLVRLNQTVIWRDQVTFSENLSTCHTKERLPSH  
930 940 950 960 970 980 990  
SDFLAELKAPVNCIAVCORIQDIPFGIOEENATLKNLSPDHYIKTSNHLILVSTABILFNDSVF  
1010 1020 1030 1040 1050 1060 1070 1080  
SDFLAELKAPVNCIAVCORIQDIPFGIOEENATLKNLSPDHYIKTSNHLILVSTABILFNDSVF  
1000 1010 1020 1030 1040 1050 1060 1070  
TLFQOGAFVSQSTETKVEPEVNPPLIVGSSVGGLLALITAAKYLGFFKQYKDMMSGGPPGABP  
1090 1100 1110 1120 1130 1140 1150  
TLFQOGAFVSQSTETKVEPEVNPPLIVGSSVGGLLALITAAKYLGFFKQYKDMMSGGPPGABP  
1070 1080 1090 1100 1110 1120 1130  
X  
O  
O  
O  
X

4. US-09-902-481B-1 (1-1153)  
US-09-902-481B-3 Sequence 3, Application US/09902481B  
Sequence 3, Application US/09902481B  
GENERAL INFORMATION:  
APPLICANT: Springer, Timothy  
APPLICANT: Shimooka, Motomu  
APPLICANT: Shifman, Julia  
APPLICANT: Mayo, Stephen  
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY  
FILE REFERENCE: A-70586-1/RPT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/902,481B  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/216,600  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 1137  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
Initial Score = 1124 Optimized Score = 1124 Significance = -1.08  
Residue Identity = 98% Matches = 1124 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0  
10 X 20 30 40 50 60 70  
MALRVLLLTALTICHFNLDTNAMTFQENARGQSVVQLOGSRVVGAPQEIIVAAKORGLYOCDDYSTGS  
FNLDNTAMTFQENARGQSVVQLOGSRVVGAPQEIIVAAKORGLYOCDDYSTGS  
X 10 20 30 40 50

80 90 100 110 120 130 140  
CEPIRLQVPEAVNMSIGLSLAFTSPPOLLAGCPVTHQTCSENTVVKGLCFGLGNLRQOPKPFPEALRGC  
CEPIRLQVPEAVNMSIGLSLAFTSPPOLLAGCPVTHQTCSENTVVKGLCFGLGNLRQOPKPFPEALRGC  
60 70 80 90 100 110 120  
PQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMBQKSKTLFSLMOYSEEFRIHFTFKFQNNPNSRLVK  
150 160 170 180 190 200 210  
PQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMBQKSKTLFSLMOYSEEFRIHFTFKFQNNPNSRLVK  
130 140 150 160 170 180 190 200  
PITQLLGRTHATGLRVKVEELFNIENGARKNAFKILFILLTDGKEGDPGLGYEDVPELDRGVIRYVLF  
210 220 230 240 250 260 270  
PITQLLGRTHATGLRVKVEELFNIENGARKNAFKILFILLTDGKEGDPGLGYEDVPELDRGVIRYVLF  
220 230 240 250 260 270 280  
DAFRSEKSRQELNTIASKPRDHFVQNNPEALKTIONQLREKIFAIEGTQTSSSSFEHMSQBSAAT  
290 300 310 320 330 340 350 360  
DAFRSEKSRQELNTIASKPRDHFVQNNPEALKTIONQLREKIFAIEGTQTSSSSFEHMSQBSAAT  
280 290 300 310 320 330 340  
SNPGLLSTVGSYDWAGGVFLYTSKESKSTFINMTRVDSMDMDAYLGAAAIILNRRVQSLVGLGAPRYOHILV  
370 380 390 400 410 420 430  
SNPGLLSTVGSYDWAGGVFLYTSKESKSTFINMTRVDSMDMDAYLGAAAIILNRRVQSLVGLGAPRYOHILV  
350 360 370 380 390 400 410  
AMFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYETGTRGQSVVCLPQCORARW  
440 450 460 470 480 490 500  
AMFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYETGTRGQSVVCLPQCORARW  
420 430 440 450 460 470 480  
QCDVAVLYGEGQPGWRFGAALTVDGLVNGDKLTDVAIGAPGEDNRCGAVLFGTSGSISPSHSQIAGSK  
510 520 530 540 550 560 570  
QCDVAVLYGEGQPGWRFGAALTVDGLVNGDKLTDVAIGAPGEDNRCGAVLFGTSGSISPSHSQIAGSK  
490 500 510 520 530 540 550 560  
LSPLRQYFGQSLSGQDLTMDGLVDLTGGAQGHVLLLRQSVLRVKAIMEFNFREAVARNVFECDQVVRGKE  
580 590 600 610 620 630 640  
LSPLRQYFGQSLSGQDLTMDGLVDLTGGAQGHVLLLRQSVLRVKAIMEFNFREAVARNVFECDQVVRGKE  
570 580 590 600 610 620 630  
AGEVRVCLHVKQSTRDLRBCQIQSVVYTDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQLP  
650 660 670 680 690 700 710 720  
AGEVRVCLHVKQSTRDLRBCQIQSVVYTDLALDSGRPHSRAVFNETKNSTRQTVLGTQTCETLKLQLP  
630 640 650 660 670 680 690 700  
NCIEDPVSPIVRLNFSVLGTPLSAGNRLVLAEDAQRLLTALPPEKCKGNDNICQDDLSITFSPMSLDC  
730 740 750 760 770 780 790  
NCIEDPVSPIVRLNFSVLGTPLSAGNRLVLAEDAQRLLTALPPEKCKGNDNICQDDLSITFSPMSLDC  
710 720 730 740 750 760 770  
LVVGGPRFNVTVVRNDGDSYRTQVTFPPFLDLSYRKVSTLQNSQSRWRLACESASSTEVSGALKSTS  
800 810 820 830 840 850 860  
LVVGGPRFNVTVVRNDGDSYRTQVTFPPFLDLSYRKVSTLQNSQSRWRLACESASSTEVSGALKSTS  
780 790 800 810 820 830 840  
CSINHIPPENSEVTNITFDVDSKASIGNKLLKANVTSENNPRNTKTFQLELPVKYAVYVWVTHSGVS  
870 880 890 900 910 920 930  
CSINHIPPENSEVTNITFDVDSKASIGNKLLKANVTSENNPRNTKTFQLELPVKYAVYVWVTHSGVS  
850 860 870 880 890 900 910 920

940 950 960 970 980 990 1000  
TKYLNFTASNTSRVNMCHQVNSNLGORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP  
TKYLNFTASNTSRVNMCHQVNSNLGORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP  
TKYLNFTASNTSRVNMCHQVNSNLGORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP  
930 940 950 960 970 980 990  
1010 1020 1030 1040 1050 1060 1070 1080  
SDFLAELRKAPVNVCSIAVCQRIQCDIPFFGIOEEFNATLKGNSLFDWYIKTSHNHLIVSTAELFND  
SDFLAELRKAPVNVCSIAVCQRIQCDIPFFGIOEEFNATLKGNSLFDWYIKTSHNHLIVSTAELFND  
SDFLAELRKAPVNVCSIAVCQRIQCDIPFFGIOEEFNATLKGNSLFDWYIKTSHNHLIVSTAELFND  
1000 1010 1020 1030 1040 1050 1060  
1090 1100 1110 1120 1130 1140 1150  
TLPLPGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMSEGGPPGAEP  
TLPLPGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMSEGGPPGAEP  
TLPLPGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMSEGGPPGAEP  
1070 1080 1090 1100 1110 1120 1130

x  
Q  
Q  
Q  
x





```
|||||
US-09-902- 412 HIGLVAMFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
US-09-902- 412 HIGLVAMFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
US-09-902- 428 HIGLVAMFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
consensus hlglvamfrqntgmwesanvkgtdqigayfgaslcsvdvdsngsdlvligaphyyeqtrg
.
US-09-902- 1
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVAVLYGEOQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVAVLYGEOQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVAVLYGEOQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVAVLYGEOQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 489 GQVSVCPLPRGQARWQCDVAVLYGEOQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
consensus gqvsvcplprgqrarwqcdavlygeogqpwgrfgaaltvlgdvngdkltdvaigapgeedn
|||||
US-09-902- 1
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGOSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGOSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGOSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGOSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 550 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGOSLSGGQDLTMDGLVDLTVGAQGHV
|||||
consensus rgavylfhgtsgsgispshsoriagsklsprlqyfgqslsggqdltdmdglvdltvgaqghv
|||||
US-09-902- 1
|||||
US-09-902- 595 LLRSQPVLRVKAIMENPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMENPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMENPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMENPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 611 LLRSQPVLRVKAIMENPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
consensus lllrsgpvlrvkaimenprevarnvfeecdqvvkgeagevrvcclhvqkstrdlrregqi
|||||
US-09-902- 1
|||||
US-09-902- 656 QSVVYDLDLSDGRPHRAVFNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLSDGRPHRAVFNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLSDGRPHRAVFNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLSDGRPHRAVFNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 672 QSVVYDLDLSDGRPHRAVFNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
consensus qsvvtydldldsgprhsvfnvnetkstrqtqvlgtqtcetlklqlpnciedpvsplv
|||||
US-09-902- 1
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALFPFKKNCNDNICODDLSITFSFMSLDCL
```

```
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALFPFKKNCNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALFPFKKNCNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALFPFKKNCNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 733 RLNFSLVGTPLSAFGLNRPVLAEDAQRLLFTALFPFKKNCNDNICODDLSITFSFMSLDCL
|||||
consensus rlnfslvgtpclsaafgnlrpvlaedaqrllftalfpfekncgndnicqddlsitfsfmsldcl
|||||
US-09-902- 1
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
US-09-902- 794 VVGGRPREFNVTVTVRNDGEDSYRTQVTFPPFPDLDLSYRKVSTLQNRORSRHLACESASST
|||||
consensus vvggprefnvtvtrndgedsyrtqvtfffpdldlsyrkvstlqnrqrsrwlacesasst
|||||
US-09-902- 1
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 855 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
consensus evsgalkstscsinhpifpensevtfnitfdvdskaslgnkllkanvtseunmptnkte
|||||
US-09-902- 1
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 916 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
consensus fglelpvkvyavvmvvtshgvstkylnfntasentsrvmqhqvsnlqorslpslsvflvpv
|||||
US-09-902- 1
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
US-09-902- 977 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAELRKAPVNVNCSIAVCORIQCDIPF
|||||
consensus rlnqtvindrpovtfsenlssctchtkerlpsshdflaelrkapvvnvncsiavcqrqcdipf
|||||
US-09-902- 1
|||||
```

```
US-09-902- 1022 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
US-09-902- 1038 FGIQEEFNATLKGNLSPDWIKTSHNHLLIVSTAEILFNDVSFTLLPGQGFVRSQETKV
|||||
consensus fgiqeefnatlkgnlsfdwyiktshnhllivstaeilfndsvftllpgggafvrsqetkv

US-09-902- 1 mgxxxxGGPP
|||||
US-09-902- 1083 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1099 EPFEVPNPPLIVGSSVGGHLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
consensus epfevpnpplivgssvvgglllallitaalyklgffkrykdmmsGGPPgaeppq
```

Alignment score = -1505.00

Scoring matrix:

	1	2	3	4	5	6
1		1044	1048	1049	1053	-5711
2			1131	1124	1122	-5631
3				1129	1126	-5631
4					1127	-5631
5						-5631
6						